

OIPE

DATE: 08/14/2001 RAW SEQUENCE LISTING TIME: 12:13:52 PATENT APPLICATION: US/09/853,033

Input Set : A:\65691222.app

Output Set: N:\CRF3\08142001\1853033.raw



Output Set: N: (CRF3 (VVIII)														
3 <110> APPLICANT: CHAMBON, PIERRE 4 METZGER, DANIEL ROPERTED RECORDER TO BE TARGETED RECORDER TO BE	OMBINATION													
6 <120> TITLE OF INVENTION: TRANSGENIC MOUSE FOR TARGETED RESOLUTION														
7 MEDIATED BY MODIFIED CRE-ER														
2 120 BILE PEEPPENCE: 065691/0222														
11 -140 CURRENT APPLICATION NUMBER. 03/033/030														
40 4141 CUIDDENT FILING DATE: 2001 05 11														
14 <150> PRIOR APPLICATION NUMBER: FR 00/123/0														
15 <151> PRIOR FILING DATE: 2000-10-03														
17 <160> NUMBER OF SEQ ID NOS: 14														
19 <170> SOFTWARE: PatentIn Ver. 2.1														
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23 <212> TIPE. DMX 24 <213> ORGANISM: Homo sapiens														
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27 <221> NAME/KEY: CDS														
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	u His													
32 Met Thr Met Thr Leu His Thr Lys Ald Set City Hos II	5													
33 1 5 cm star gag gag ctg aac cgt ccg cag ct	c aag 96													
35 cag atc caa ggg aac gag ctg gag ctc ctg dab sy 35 cag atc caa ggg aac gag ctg gag ctc ctg dab sy 35 atc and	u Lys													
37 20 25 39 atc ccc ctg gag cgg ccc ctg ggc gag gtg tac ctg gac agc ag 39 atc ccc ctg gag cgg ccc ctg ggc gag gtg tac ctg gac agc ag	c aag 144													
39 atc ccc ctg gag cgg ccc ctg ggc gag gcg cas de s 40 Ile Pro Leu Glu Arg Pro Leu Gly Glu Val Tyr Leu Asp Ser Se	r Lys													
40 Tie Pio fieu ord firs 45 41	c gcc 192													
The same and and and the day lie as	e gee 192													
AA Dro Ala Val Tvr ASh Tvi Plo Giu Gij Mid1	II ALG													
44 PIO AIR VAL 171 1151 11 55 60 45 50 55 55 60 60 60 60 60 60 60 60 60 60 60 60 60	ec tac 240													
45 50 50 47 gcg gcc gcc aac gcg cag gtc tac ggt cag acc ggc ctc cc	o Tyr													
48 Ala Ala Ala Ash Ash Gin Val 191 Gi, 375	80													
49 65 /U	gg ggt 288													
51 ggc ccc ggg tct gag gct gcg gcg ttc ggc coo and 35 52 Gly Pro Gly Ser Glu Ala Ala Ala Phe Gly Ser Asn Gly Leu Gl	Ly Gly													
of and contact of the	tg cac 336													
ac at the pro ton Ach Ser val Set Fio Det 110 -	eu His													
by and the charge age can ear ear ear ear ear ear ear ear	ag gtg 304													
co pro pro Cln Leil Ser Pro Pile Leu Gin 110 111	III Vai													
61 115 120 63 ccc tac tac ctg gag aac gag ccc agc ggc tac acg gtg cgc gag 63 ccc tac tac ctg gag aac gag ccc agc ggc tac acg gtg cgc gag 63 ccc tac tac ctg gag aac gag ccc agc ggc tac acg gtg cgc gag 63 ccc tac tac ctg gag aac gag ccc agc ggc tac acg gtg cgc gag	lu Ala													
64 Pro Tyr Tyr Leu Glu Ash Glu Plo Sel Gly 172	-													
65 130 133 67 ggc ccg ccg gca ttc tac agg cca aat tca gat aat cga cgc c	<u> </u>													

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Output Set: N:\CRF3\08142001\I853033.raw

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68 Gly Pro Pro	Ala Phe T	yr Arg F	ro Asn	Ser Asp	Asn Arg	Arg Gln	GLY	
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	aga ttg g	rcc agt a	acc aat	gac aag	gga agt	atg gct	Mot	320
71 ggc aga gaa 72 Gly Arg Glu	Arg Leu A	la Ser 1	thr Asn	ASP DAS	Gly Ser	175	Mec	
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	aag gag a	ict cgc t	tac tgt	gca gtg	f tgc aac	Asp Tyr	Ala	3,0
75 gaa tet gee 76 Glu Ser Ala	Lys Glu T	hr Arg	ryr cys	Ala Val	Cys Asii	190		
								624
77 79 tca ggc tac	cat tat o	gga gtc	tgg tcc	Cyc Clu	g gge ege i Glv Cvs	Lvs Ala	Phe	
80 Ser Gly Tyr	His Tyr (STA Agr	Trp Ser	Cys Gic	205	-1-		
								672
81 195 83 ttc aag aga 84 Phe Lys Arg	agt att	caa gga	uic Nen	Asp Tvi	r Met Cys	Pro Ala	Thr	
	Ser Ile	215 215	HIS WOLL	nsp 112	220			
85 210 87 aac cag tgc			aac agg	agg aag	age tge	cag gcc	tgc:	720
87 aac cag tgc 88 Asn Gln Cys	acc att	yat ada Nan Twa	aac ayy Asn Ard	Arg Ly	s Ser Cys	Gln Ala	Cys	
89 225 91 cgg ctc cgc			ata aga	atg at	g aaa ggt	ggg ata	ı cga	768
91 cgg ctc cgc 92 Arg Leu Arg	add Lyc	Tyr Glu	Val Gly	Met Me	t Lys Gly	g Gly Ile	e Arg	
93 95 aaa gac cga		agg aga	atg tto	aaa ca	c aag cgc	c cag aga	a gat	816
95 aaa gac cga 96 Lys Asp Arg	aga gga Ara Glv	Glv Arg	Met Le	1 Lys Hi	s Lys Arg	g Gln Arq	g Asp	
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97 99 gat ggg gag		ggt gāā	gtg ggg	g tot go	t gga gad	c atg aga	gct	864
99 gat ggg gag 100 Asp Gly Gl	n Glv Arq	Gly Glu	val G	Ly Ser A	u		rg Ala	
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101		agc ccg	g ctc a	tg atc a	aa cgc to	ct aag a	ag aac	912
103 gcc aac ct 104 Ala Asn Le	eu Trp Pro	Ser Pro	Leu M	et Ile I	170	er Lys L	ys Asii	
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	cc ttg tcd	ctg acq	g gcc g	ac cag a	itg gtc a	gt gee t	ou Leu	,,,,
107 agc ctg go 108 Ser Leu A	la Leu Sei	c Leu Thi	r Ala A	sh am	100 /41 -	er vra n	320	
								1008
109 305 111 gat gct ga	ag ccc ccc	c ata ct	c tat t	cc gag u	Lat yat C	ro Thr A	ra Pro	
111 gat gct ga 112 Asp Ala G	lu Pro Pro	o Tre re	u Tyr S	er Giu i 330	LYL ASP 1	3	35	
								1056
113 115 ttc agt g	aa gct tc	g atg at	g ggc L	ou Lou	Thr Asn L	eu Ala A	sp Arg	
115 ttc agt g 116 Phe Ser G	lu Ala Se	r met me	r Gra n	45		350	-	
117 119 gag ctg g	340		a +aa a	og aag a	aga ata c	ca qqc t	tt gtg	1104
119 gag ctg g 120 Glu Leu V	tt cac at	g atc aa	n Trn A	la Lvs /	Arg Val P	ro Gly F	he Val	
	55	+ ~n+ na	~ ~+ ~ ~	ac ctt.	cta gaa t	gt gcc t	gg cta	1152
123 gat ttg a 124 Asp Leu T	CC CTC Ca	t gat ca	n Val F	is Leu	Leu Glu C	ys Ala T	rp Leu	
125 370 127 gag atc c			a ata t	aa cac	tcc atg c	gag cac o	cca ggg	1200
127 gag atc o 128 Glu Ile I	ug alg al	a Clarte	u Val 1	rp Arg	Ser Met G	Glu His I	ro Gly	•
129 385 131 aag cta c	+ - +++		ac tta o	ctc ttg	gac agg a	ac cag	gga aaa	1248
131 aag cta o 132 Lys Leu I	on pho x1	a Pro As	n Leu l	Leu Leu	Asp Arg A	Asn Gln (Gly Lys	}
132 Lys Leu I	led the vi							

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133	410 415	
136 Cys Val Glu Gly Met Val Glu He File Pile App		t.ca 1296
136 Cys Val Glu Gly Met Val Glu He File Pile App	135 tgt gta gag ggc atg gtg gag atc ttc gac atg ctg ctg gcc atg	Ser
139 tct cgg atg atg aat ctg cag gag gag gag gag gag gag gag gag ga	136 Cys Val Glu Gly Met Val Glu Tie File Asp Met Bet 2430	
140 Ser Arg Phe Arg Met Met Ash Leu On 1619 of 445 141		
140 Ser Arg Phe Arg Met Met Ash Leu On 1619 of 445 141	139 tot egg tte ege atg atg aat etg eag gga gag gag ete gag egg	Leu
141 435 143 aaa tct att att ttg ctt aat tct ggg gtg tac aca ttt ctg tcc agc 1392 144 Lys Ser Ile Ile Leu Leu Asn Ser Gly Val Tyr Thr Phe Leu Ser Ser 455 145 450 147 acc ctg aag tct ctg gaa gag aag gac cat atc cac cga gtc ctg gac 148 Thr Leu Lys Ser Leu Glu Glu Lys Asp His Ile His Arg Val Leu Asp 470 148 Thr Leu Lys Ser Leu Glu Glu Lys Asp His Ile His Arg Val Leu Asp 480 151 aag atc aca gac act ttg atc cac ctg atg gcc aag gca gcc ctg acc 151 aag atc aca gac cac cag cgg ctg acc 152 Lys Ile Thr Asp Thr Leu Ile His Leu Met Ala Lys Ala Gly Leu Thr 485 155 ctg cag cag cag cac cag cgg ctg gcc cag ctc ctc ctc atc ctc tcc 156 Leu Gln Gln His Gln Arg Leu Ala Gln Leu Leu Leu Ile Leu Ser 500 159 cac atc agg cac atg agt aac aaa agg ac atg gag cat ctg tac agc atg 1584 160 His Ile Arg His Met Ser Asn Lys Gly Met Glu His Leu Tyr Ser Met 616 515 163 aag tgc aag aac gtg gtg ccc ctc tat gac ctg ctg gag atg ctg 1632 164 Lys Cys Lys Asn Val Val Pro Leu Tyr Asp Leu Leu Leu Glu Met Leu 165 530 167 gac gcc cac cgc cta cat gcg cca act gcg gtg gag ggg gga ggg gga ggg gg gg gg gg gg	140 Ser Arg Phe Arg Met Met Ash Leu Gin Gly Gia Gia 145	
144 Lys Ser Ile Ile Leu Leu Ash Ser Gry Vat		
144 Lys Ser Ile Ile Leu Leu Ash Ser Gry Vat	143 aaa tot att att ttg ott aat tot gga gtg tae dea tot org	Ser
145	144 Lys Ser Ile Ile Leu Leu Ash Ser Gly var 191 144 A60	
148 Thr Leu Lys Ser Leu Glu Glu Lys App		gac 1440
149 465 151 aag atc aca gac act ttg atc cac ctg atg gcc aag gcc ag gcc ctg acc	147 acc ctg aag tot ctg gaa gag aag gae cut dee out ag	Asp
149 465 151 aag atc aca gac act ttg atc cac ctg atg gcc aag gcc ctg acc 152 Lys Ile Thr Asp Thr Leu Ile His Leu Met Ala Lys Ala Gly Leu Thr 153 485 155 ctg cag cag cac cac cag cgg ctg gcc cag ctc ctc ctc atc ctc 1536 155 ctg cag cag cac cac cag cgg ctg gcc cag ctc ctc ctc atc ctc 156 Leu Gln Gln His Gln Arg Leu Ala Gln Leu Leu Ile Leu Ser 157 500 500 159 cac atc agg cac atg agt aac aaa ggc atg gag cat ctg tac agc agc atg ag ag cac ctg ctg ctg gcc 160 His Ile Arg His Met Ser Asn Lys Gly Met Glu His Leu Tyr Ser Met 161 515 520 520 520 163 aag tgc aag aac gtg gtg ccc ctc tat gac ctg ctg gag atg gtg ccc 164 Lys Cys Lys Asn val Val Pro Leu Tyr Asp Leu Leu Leu Glu Met Leu 165 530 167 gac gcc cac cgc cta cat gcg ccc act agc gtg gga ggg gca tcc gtg 168 Asp Ala His Arg Leu His Ala Pro Thr Ser Arg Gly Gly Ala Ser Val 169 545 550 550 550 171 gag gag acg gac caa agc cac ttg gcc act gcg ggg gct ct act tca tcg 172 Glu Glu Thr Asp Gln Ser His Leu Ala Thr Ala Gly Ser Thr Ser Ser 173 565 575 575 175 cat tcc ttg caa aag tat tac atc acg ggg gag gag ggg ggg ggg ggg ggg gg		480
152 Lys 1le Thr Asp 485 490 495 485 485 490 485 490 485	149 465	acc 1488
153	151 aag atc aca gac act tig atc cac ctg des soon as	Thr
153 ctg cag cag cag cac cag cgg ctg gcc cag ctc ctc ctc atc ctc tcc 1536 155 ctg cag cag cag cac cac cag cgg ctg gcc cag ctc ctc ctc atc ctc tcc 1536 156 Leu Gln Gln Gln His Gln Arg Leu Ala Gln Leu Leu Leu Ile Leu Scr 510 157		
156 Leu Gln Gln Gln His Gln Arg 150	153 and agg etg got cag etc etc etc ate etc	tcc 1536
157	155 ctg cag cag cag cac cag cyg ctg goo day	Ser
157		
160 His Ile Arg His Met Ser Ash Lys Gly Met Ct	157 300 and and ago at gag cat ctg tac ago	atg 1584
161	159 cac atc agg cac atg age tale and sylven Met Glu His Leu Tyr Ser	Met
163 aag tgc aag aac gtg gtg ccc ctc tat gac ctg ctg gag atg ctg 164 Lys Cys Lys Asn Val Val Pro Leu Tyr Asp Leu Leu Leu Glu Met Leu 165 530 535 540 167 gac gcc cac cgc cta cat gcg ccc act agc cgt gga ggg gca tcc gtg 168 Asp Ala His Arg Leu His Ala Pro Thr Ser Arg Gly Gly Ala Ser Val 169 545 550 550 560 171 gag gag acg gac caa agc cac ttg gcc act gcg ggc tct act tca tcg 172 Glu Glu Thr Asp Gln Ser His Leu Ala Thr Ala Gly Ser Thr Ser Ser 173 565 570 570 175 cat tcc ttg caa aag tat tac atc acg ggg gag gag gag ggg ttc cct 176 His Ser Leu Gln Lys Tyr Tyr Ile 177 580 179 gcc aca gtc tga 180 Ala Thr Val 181 595 184 <210> SEQ ID NO: 2 185 <211> LENGTH: 595 186 <212> TYPE: PRT 187 <213> ORGANISM: Homo sapiens 189 <400> SEQUENCE: 2 190 Met Thr Met Thr Leu His Thr Lys Ala Ser Gly Met Ala Leu Leu His 191 1 5 10 15 10 15 10 15 110 110 110 110 110 110 111 110 110 1		
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165 530 535 535 535 535 660 167 gac gcc cac cgc cta cat gcg ccc act agc cgt gga ggg gca tcc gtg 1680 168 Asp Ala His Arg Leu His Ala Pro Thr Ser Arg Gly Gly Ala Ser Val 550 550 550 560 171 gag gag acg gac caa agc cac ttg gcc act gcg ggc tct act tca tcg 1728 172 Glu Glu Thr Asp Gln Ser His Leu Ala Thr Ala Gly Ser Thr Ser Ser 570 575 575 173 565 175 cat tcc ttg caa aag tat tac atc acg ggg gag gca gag ggt ttc cct 1776 176 His Ser Leu Gln Lys Tyr Tyr Ile Thr Gly Glu Ala Glu Gly Phe Pro 177 580 585 590 1788 180 Ala Thr Val 181 595 184 <210> SEQ ID NO: 2 185 <211> LENGTH: 595 186 <212> TYPE: PRT 187 <213> ORGANISM: Homo sapiens 189 <400> SEQUENCE: 2 190 Met Thr Met Thr Leu His Thr Lys Ala Ser Gly Met Ala Leu Leu His 191 1 5 10 15 15 193 Gln Ile Gln Gly Asn Glu Leu Glu Pro Leu Asn Arg Pro Gln Leu Lys 194 20 196 Ile Pro Leu Glu Arg Pro Leu Gly Glu Val Tyr Leu Asp Ser Ser Ser Lys 145	163 aag tgc aag aac geg geg soo bell Tyr Asp Leu Leu Glu Met	Leu
167 gac gcc cac cgc cta cat gcg ccc act agc cgt gga ggg ggd gca tcc ycg 168 Asp Ala His Arg Leu His Ala Pro Thr Ser Arg Gly Gly Ala Ser Val 169 545 171 gag gag acg gac caa agc cac ttg gcc act gcg ggc tct act tca tcg 172 Glu Glu Thr Asp Gln Ser His Leu Ala Thr Ala Gly Ser Thr Ser Ser 173 565 175 cat tcc ttg caa aag tat tac atc acg ggg gag gag gag ggt ttc cct 176 His Ser Leu Gln Lys Tyr Tyr Ile Thr Gly Glu Ala Glu Gly Phe Pro 177 580 179 gcc aca gtc tga 180 Ala Thr Val 181 595 184 <210> SEQ ID NO: 2 185 <211> LENGTH: 595 186 <212> TYPE: PRT 187 <213> ORGANISM: Homo sapiens 189 <400> SEQUENCE: 2 190 Met Thr Met Thr Leu His Thr Lys Ala Ser Gly Met Ala Leu Leu His 191 1 193 Gln Ile Gln Gly Asn Glu Leu Glu Pro Leu Asn Arg Pro Gln Leu Lys 194 20 196 Ile Pro Leu Glu Arg Pro Leu Gly Glu Val Tyr Leu Asp Ser Ser Lys		
168 Asp Ala His Arg Leu His Ara Pro Int Set 555 560 169 545 550 550 560 171 gag gag acg gac caa agc cac ttg gcc act gcg ggc tct act tca tcg 1728 172 Glu Glu Thr Asp Gln Ser His Leu Ala Thr Ala Gly Ser Thr Ser Ser 575 173 565 570 575 175 cat tcc ttg caa aag tat tac atc acg ggg gag gca gag ggt ttc cct 1776 176 His Ser Leu Gln Lys Tyr Tyr Ile Thr Gly Glu Ala Glu Gly Phe Pro 580 179 gcc aca gtc tga 180 Ala Thr Val 181 595 184 <210> SEQ ID NO: 2 185 <211> LENGTH: 595 186 <212> TYPE: PRT 187 <213> ORGANISM: Homo sapiens 189 <400> SEQUENCE: 2 190 Met Thr Met Thr Leu His Thr Lys Ala Ser Gly Met Ala Leu Leu His 191 1 191 1 5 193 Gln Ile Gln Gly Asn Glu Leu Glu Pro Leu Asn Arg Pro Gln Leu Lys 194 20 25 196 Ile Pro Leu Glu Arg Pro Leu Gly Glu Val Tyr Leu Asp Ser Ser Lys	-t- art aga aga aga aga aga aga aga aga aga ag	gtg 1680
1728 171 gag gag acg gac caa agc cac ttg gcc act gcg ggc tct act tca tcg 172 Glu Glu Thr Asp Gln Ser His Leu Ala Thr Ala Gly Ser Thr Ser Ser 173	169 Agn Ala His Arg Leu His Ala Pro Thr Ser Arg Gly Gly Ala Ser	· Val
171 gag gag acg gac caa agc cac ttg gcc act ggg ggc tet act colors 172 Glu Glu Thr Asp Gln Ser His Leu Ala Thr Ala Gly Ser Thr Ser Ser 173		
172 Glu Glu Thr Asp Gln Ser His Leu Ala Interval 173 565 575 173 565 570 570 575 175 cat tcc ttg caa aag tat tac atc acg ggg gag gca gag ggt ttc cct 176 His Ser Leu Gln Lys Tyr Tyr Ile Thr Gly Glu Ala Glu Gly Phe Pro 580 585 585 590 179 gcc aca gtc tga 180 Ala Thr Val 181 595 184 <210> SEQ ID NO: 2 185 <211> LENGTH: 595 186 <212> TYPE: PRT 187 <213> ORGANISM: Homo sapiens 189 <400> SEQUENCE: 2 190 Met Thr Met Thr Leu His Thr Lys Ala Ser Gly Met Ala Leu Leu His 191 1 5 193 Gln Ile Gln Gly Asn Glu Leu Glu Pro Leu Asn Arg Pro Gln Leu Lys 30 194 20 25 30 196 Ile Pro Leu Glu Arg Pro Leu Gly Glu Val Tyr Leu Asp Ser Ser Lys 45	and the ecc act acc acc acc	tcg 1/20
173	172 Glu Glu Thr Asp Gln Ser His Leu Ala Thr Ala Gly Ser Thr Ser	ser
175 cat tcc ttg caa aag tat tac atc acg ggg gag gca ga		
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191 1 5 193 Gln Ile Gln Gly Asn Glu Leu Glu Pro Leu Asn Arg Pro Gln Leu Lys 193 Gln Ile Gln Gly Asn Glu Leu Glu Pro Leu Asn Arg Pro Gln Leu Lys 194 25 30 194 25 45		5
194 20 23 196 Ile Pro Leu Glu Arg Pro Leu Gly Glu Val Tyr Leu Asp Ser Ser Lys	191 1 5 The Gly Ley Cly Pro Ley Ash Arg Pro Gln Le	u Lys
194 20 196 Ile Pro Leu Glu Arg Pro Leu Gly Glu Val Tyr Leu Asp Ser Ser Lys 45		
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197 35 199 Pro Ala Val Tyr Asn Tyr Pro Glu Gly Ala Ala Tyr Glu Phe Asn Ala		
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	199 Pro Ala val Tyl Ash Tyl 120 ola 3-1	

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2	05	C1v	Dro	G1v	Sar	Glu		Δla	Ala	Phe	Glv	Ser	Asn	Gly	Leu	Gly	Gly
		СТУ	FIO	GLY	JCI	85	21.1.4				90			•		95	_
_	206	Dho	Dro	Dro	Tou		Sar	Val	Ser	Pro		Pro	Leu	Met	Leu	Leu	His
		Pile	PIO	PIO	100	N311	JCI	, u i	001	105					110		
_	209	D	Desc	Dwo	T00	T OU	Cor	Dro	Dho		Gln	Pro	His	Glv	Gln	Gln	Val
		Pro	Pro		GIII	Leu	261	FIO	120	ncu	0111	110	1110	125	<u> </u>		
2	212	_		115	T	C1	7 an	Clu		Car	C1v	ጥህዮ	Thr		Arg	Glu	Ala
		Pro		TAL	ьeu	GIU	ASII	135	FIO	JCI	GLY	-1-	140	,	9		
2	215		130	_	. 1 -	Db -	ìm		Dwo	Nan	cor	λen		λrα	Δra	Gln	Glv
			Pro	Pro	Ата	Phe		Arg	PIO	ASII	261	155	LOII	пта	Arg	0111	160
2	218	145			_	_	150	a	m la sa	N a n	N a ro		C137	cor	Mot	λla	
		Gly	Arg	GLu	Arg		Ата	ser	THE	ASII	170	гу	СТУ	Ser	Met	175	ricc
2	221			_		165	_,		m	G		3701	Crra	7 an	A cn		λla
		Glu	Ser	Ala		Glu	Thr	Arg	Tyr		Ald	Val	Cys	ASII	Asp 190	1 Y 1	AIG
2	224				180				_	185	G	a 1	<i>α</i> 1	0		λla	Dho
2	226	Ser	Gly		His	Tyr	Gly	Val	Trp	ser	Cys	GIU	СТУ	205	Lys	Ата	FILE
7	227			195			_		200	_	_	m	36-4		Dance	7 J o	mh~
7	229	Phe		Arg	Ser	Ile	GIn		HlS	Asn	Asp	туг	met	Cys	Pro	нта	TIIT
7	230		210					215	_	_	_		220	a	a 1-	3 1 5	Ctra
			Gln	Cys	Thr	Ile		Lys	Asn	Arg	Arg	гуs	ser	Cys	Gln	Ата	240
- 2	233	225					230					235	T	01. .	01	тіс	
		Arg	Leu	Arg	Lys		Tyr	GLu	Va⊥	GTĀ	Met	мет	гăг	GTĀ	Gly	116	Arg
2	236					245				_	250	77.1 m	T	7	C1 n	255	A an
	238	Lys	Asp	Arg		Gly	Gly	Arg	Met	Leu	Lys	HIS	гàг	Arg	Gln	Arg	ASP
- 2	239				260		_			265	_	- 1 -	a 1	3	270	7 ~~	7.1 ~
:	241	Asp	Gly		Gly	Arg	Gly	Glu		GTA	ser	Ата	GTY	ASP	Met	AIG	Ата
:	242			275				_	280		-1.	T	3	285	T	T *** G	Agn
:	244	Ala		Leu	\mathtt{Trp}	Pro	Ser		Leu	Met	ire	гĀг		ser	Lys	гуѕ	ASII
:	245		290					295		_	01 .	34 - L	300	d = =	71-	T 011	T OU
			Leu	Ala	Leu	Ser		Thr	Ата	Asp	GIN	Met	val	ser	Ala	ьец	320
:	248	305					310		_	_	a 1	315	3	D	mh w	7 ~~	
		Asp	Ala	Glu	Pro		He	Leu	Tyr	ser	GIU	туг	ASP	PLO	Thr	335	PIO
	251			,		325				_	330	m1		+	77.		7 20
	253	Phe	Ser	Glu		Ser	Met	Met	GLY	Leu	Leu	Thr	ASI	Leu	AId	ASP	Arg
	254				340		_		_	345	_		**- 7	D	350	nho	3701
		Glu	Leu			Met	Ile	Asn	Trp	Ala	ьys	Arg	vaı	PLO	СТУ	Pile	Val
	257			355					360		-	-	a 1	365		III mm	T 011
	259	Asp	Leu	Thr	Leu	His	Asp			His	Leu	ьеu	Glu	Cys	Ala	ттр	ьец
	260		370					375			_	_	380		**! _	D	61
	262	Glu	Ile	Leu	Met	Ile		Leu	Val	Trp	Arg	Ser	мет	GIU	HIS	Pro	Gly
	263	385					390				_	395		_	a1	a 1	400
	265	Lys	Leu	Leu	Phe			Asn	Leu	Leu			Arg	Asn	GIN	GTÄ	Lys
	266					405					410		_	_		415	
	268	Cys	Val	Glu			Val	Glu	Ile	Phe	Asp	Met	Leu	Leu	Ala	rnr	Ser
	269				420					425		~ -	a 1	D 1	430		Tarr
	271	Ser	Arg	Phe	Arg	Met	Met	Asn	Leu	Gln	Gly	GLu	GLu	Phe	val	cys	Leu
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Output Set: N:\CRF3\08142001\1853033.raw

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283 Leu Gln Gln His Gln Arg Leu Ala Gln Leu Leu Ile Leu Ser
286 His Ile Arg His Met Ser Asn Lys Gly Met Glu His Leu Tyr Ser Met
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 292 Asp Ala His Arg Leu His Ala Pro Thr Ser Arg Gly Gly Ala Ser Val
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  324 Asp Ala Thr Ser Asp Glu Val Arg Lys Asn Leu Met Asp Met Phe Arg
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   328 Asp Arg Gln Ala Phe Ser Glu His Thr Trp Lys Met Leu Leu Ser Val
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   332 Cys Arg Ser Trp Ala Ala Trp Cys Lys Leu Asn Asn Arg Lys Trp Phe
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VERIFICATION SUMMARY

PATENT APPLICATION: US/09/853,033

DATE: 08/14/2001 TIME: 12:13:53

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